

OM protein - protein search, using sw model

Run on: April 26, 2003, 12:57:35 ; Search time 19 Seconds

Perfect score: 4391 Sequence: 1 MADIDVEAIIKKLTLAEKVD.....DGVALRQKFTVGETYWWMSGV 833

Scoring table: BLOSUM62 Gapopen 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100% Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB_pep:*

2: /cgn2_6/ptodata/1/iaa/SB_COMB_pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB_pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB_pep:*

5: /cgn2_6/ptodata/1/iaa/PCRS_COMB_pep:*

6: /cgn2_6/ptodata/1/iaa/bacfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96.9	22.1	769	3 US-09-320-878-12	Sequence 12, Appl
2	95.3	21.7	721	4 US-09-134-071-19	Sequence 19, Appl
3	951.5	21.7	3782	4 US-09-105-537-4	Sequence 4, Appl
4	944.5	21.5	809	4 US-09-105-537-24	Sequence 24, Appl
5	860	19.6	735	4 US-09-147-236-7	Sequence 7, Appl
6	731.5	16.7	744	2 US-08-462-080B-2	Sequence 2, Appl
7	731.5	16.7	744	3 US-08-462-090-2	Sequence 2, Appl
8	731.5	16.7	744	3 US-08-463-461-2	Sequence 2, Appl
9	433.5	9.9	804	4 US-08-931-416B-3	Sequence 3, Appl
10	132.5	3.0	328	2 US-08-600-452A-6	Sequence 6, Appl
11	128.5	2.9	2032	4 US-09-071-033-458	Sequence 458, App
12	128.5	2.9	2032	4 US-09-071-033-452	Sequence 462, App
13	128.5	2.9	2032	4 US-09-071-035-466	Sequence 466, App
14	128.5	2.9	2032	4 US-09-071-035-460	Sequence 460, App
15	122.5	2.8	737	4 US-09-071-035-460	Sequence 8, Appl
16	121.5	2.8	2647	2 US-08-779-113-8	Sequence 458, App
17	121.5	2.8	2647	2 US-08-779-113-8	Sequence 458, App
18	121	2.8	2353	4 US-09-377-153-33	Sequence 33, Appl
19	121	2.8	2353	4 US-08-913-941-4	Sequence 4, Appl
20	121	2.8	2353	4 US-09-659-974-33	Sequence 33, Appl
21	121	2.8	2411	4 US-09-172-341-36	Sequence 36, Appl
22	118.5	2.7	599	2 US-08-172-341B-4	Sequence 4, Appl
23	118.5	2.7	599	2 US-09-032-315-6	Sequence 6, Appl
24	118.5	2.7	599	2 US-09-093-318A-6	Sequence 6, Appl
25	118.5	2.7	599	4 US-09-399-886-6	Sequence 6, Appl
26	118.5	2.7	599	4 US-09-316-260-6	Sequence 6, Appl
27	118.5	2.7	599	4 US-09-316-281-6	Sequence 6, Appl

RESULT 1
US-09-320-878-12
; Sequence 12, Application US/09320878A
; Patient No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: McDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 3006220120
; CURRENT APPLICATION NUMBER: US/09/3200, 878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141, 908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073, 538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846, 247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119, 139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100, 880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087, 080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: patentin Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
; US-09-320-878-12

Query Match Similarity 22.1%; Score 969; DB 3; Length 769; Best Local Similarity 32.6%; Pred. No. 1.4e-86; Matches 277; Conservative 112; Mismatches 340; Indels 120; Gaps 25;

OY 13 LTLAAEKLVLLAGIDFW-----HTKALPKHGVPSLRFTDOPNGVKGTKFENGVPA 62
Db 1 MTLDKEKSFV---HWALDPDRQNNGYLPGVPRLGIPEDLRADGPNGIR--LVGQTAT 52

OY 63 CFPCCPISLGISIFNQNTLEEGKGKMGEAKASAAVILGTITNNMSPUGGRGESIGDP 122
Db 53 ALPPAPVALASTPDDFMKVKMGRDGRALNQDNODVKGPMNNTRPHGRNTEFSEDP 112

OY 123 FLAGGAALIRGIOSTGVQATIKHFLCNQDERRMMVOSIVTERALREIVALPQIAR 182
Db 113 LVSSRRAVAGIQKGQAGLMTTAKHAANNQENNRFSVNAVNDEQTLREIFPRAE-ASS 171

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/949,026
 FILING DATE: 10-OCT-1997
 APPLICATION NUMBER: 60/056,916
 FILING DATE: 05-DEC-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REFERENCE/DOCKET NUMBER: 38-347
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 858-677-1456
 TELEFAX: 858/677-1465

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
 LENGTH: 721 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-134-078-19

Query Match 21.7%; Score 953; DB 4; Length 721;
 Best Local Similarity 30.3%; Pred. No. 4.6e-85;
 Matches 261; Conservative 127; Mismatches 286; Gaps 25;

QY 6 VEATLKKILTAKEVUDLLLAGIDF-----WHTKALPKHGVPSLRFDPNGV 50
 Db 4 IDETLSOLTEEKVKLVVGLPGLFGNPHSRVAGAGETHPVPRLGIPAVFLADCPAGL 63

QY 51 R---GTYFNGVPAACEPCGTSLSGSTFNQTLLEAGKMMGKEALAKSAHVLGLPTINMQ 106
 Db 64 RNPTRPENTDNTYTTAPPVETLASTWNRLDLEEVKGAKMEEVREYVGVDVILLAPMNH 123

QY 107 RSPLGGRGPESTEDPFLGLGAALTRGOSTGVQATKHLCLNQDDERRMMOSIVTE 166
 Db 124 RNPLCGRMENEYSEDPVLSGEMASAFWKVGVSQGVGACKHIFVANNOETNMVOTIVE 183

QY 167 RALREIYALPPFOIAVRDSQPSGAEMTAYNGINGVSCSENPKYLDGMLRKENGWDGLIMSDN 226
 Db 184 RALREIYLKGFFELAVKARRPWTMSAYNKLNKGYCSONEWLKKVIREENGFFGFMDSN 243

QY 227 YGYSTTEAWAGDLEMGGP-----RPGETLKFNSNGKPFTHVQDRAREVLQF 279
 Db 244 YAGDNPVQBLKAGNDIMPKGAVQNTERRDEEIEAMEALKGKLSEEVILEECVRNKL 302

QY 280 VKKCAASGVPENPE--TVNTPET--AALLRKVGNEGVILKNNENNVLPLSKKK 333
 Db 303 -----VLTWNAFSFKGYYRSNKPDLIESHALEVAYENGAEGVILLEN-NSYLP'DENTHY 353

RESULT 2

US-09-134-078-19

Sequence 19, Application US/09134078
 Patent No. 6568844

GENERAL INFORMATION:

APPLICANT: Bylina, Edward J.

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

APPLICANT: Gray Cary Ware & Freidenrich LLP
 ADDRESSEE: San Diego
 STATE: CA
 COUNTRY: USA
 STREET: 4365 Executive Drive, Suite 1600
 CITY: San Diego
 ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/134,078
 FILING DATE: 13-AUG-1998
 CLASSIFICATION: 435

QY 183 DSQPGAMETAYNGINGVSCSENPKYLDGMLRKENGWDGLIMSDWGTYSSTEAVAGLQ 242
 Db 172 KAGAGSFCMCAYNGLNGKPSCONDELLNLNVRLTQWFGQWMSDWLAT-PGTDATKGLDQ 230

QY 243 EM-----POPP-RPGETLKFNSNGK-PFIHVIDQRAREVLOFVKKAASGV 288
 Db 231 ENGVELPGDVPKGEPSPPAKFGEALKTAVLINGTVEAAVTSAERTIVSGOMEKRGILLAT 290

QY 289 TENGPETVNNTIPTETALLRKVGNEGIVLKNENNVLPLS-KKKKTLVGPNAKQATYH 346
 Db 291 PAPRPE--RDKGAGAVSRKVAENGAVLRLNRQEGQALPLAGDAGKSIAVIGPATVDPKV 347

QY 347 GGGSAMARAYYAVTPPDGLSKOLETPPSYTGVAYTTPPLGECLTPGAPGMWRVN 406
 Db 348 GLGSAHVVPSDAAPIDTIKAR-----AGAGATVYETGETGFTQIPAGNLSPAFN 399

QY 407 EPPGTPNROHIDELEFTKTDMLHVDYVHPKAADTWYADEGTYTADEDTYEGLVYVGT 466
 Db 400 QC-----HOLE--PGKAGALY--DGLTAWPDGEYRRAVATG- 433

QY 467 AKAYVDDQLWVDNATKQVPGDAFFGSAATREETGRINLVKGNTYFKIERGSAPTYTLKD 526
 Db 434 -GYATVQVL---GSHTIEAQGVICKS--SPLKLTKG-TKHL-----TISCF 473

QY 527 TIVPGHGLSLRGVCKVDDOETEKSVALAKEHODVTCAGLNADWETGADRSKMLPG 586
 Db 474 AMSATPSLSELGWVTPAADATIKAVERSAKARTAVVER--XDDGTEGVDRPNLSPG 530

QY 587 VLDOLIADVAAANPNTVWAMQGTTPEEMPMDATPAVIQAWYGGNETGNSIADVFGDN 616
 Db 531 TQDKLISAVADANPNTVWLMGSSVLMPLSKTRAVDQWYPSQAGABAATAALYGDVN 590

QY 647 PSCKLISFPKRLQDNPAFLNFRTEAG-----RTLYGEDVYGRYIYERADKDVN 696
 Db 591 PSKGLQFSE-----PAAEHOVAGDPPTSYGVQDNOQTYRGEHIVGVRWERKENVRL 643

QY 697 FFGHGSYTFAFPSLUSVH-KDOKLISVLSKVNIGSTPGAVQALYKPLQAKINRP 755
 Db 644 FFGHGSYTFSTQASPTVVRTSIGLKIVTWRNSKGRAQEVOVQAGPNTAQOA 733

QY 756 VRELKFAYKELQPGTAKVITIEEQKYVAYFBERDOWCVERGKDYEVIVSPSSAAKDG 815
 Db 704 KKLKVITKVSLLAEGAKTVWNVDRQL-QFWDAATDNWKTGIGRNRLQTGSSSA--- 758

QY 816 VALRGKFTV 824
 Db 759 -DLRGSATV 766

QY 334 LIVGPNAKQATYHGGSAALARAYYAVTPDGLSKOLETPPSYTGVAYTTPPLGBQCLT 393
 Db 354 AVFGTGQETIKQGTGSGDTHPRYTISILEGIKE----- 387

QY 394 POGAPGMKWRVRFNEPPTPNRGRHIDELEFTKTDMLHVDYVHPKAADTWYADEGTYTADE 453
 Db 388 -----RMKFDDEELASTYEYIK-----MRETEEYKPR-TDSW----- 420

QY 454 DCTYELGLWVCGTAKAVDDQLVWDNATKQVPGDAFFGSAATREETGRINLVKGNTYFKI 513
 Db 421 -----GTVI---KPKLPENLSEKETIKPKPKNDVAVV-----ISRISGECYDRK- 463

QY 514 ERGSAPTYTLKGDTIVPGHSLRVGGCKVDDQETEKSVALAKE-HDQYTCAGLNADW 572
 Db 464 -----PVKGDFYLS-----DDELELIKV-SKEFHQD----- 489

QY 573 ETEGADRASKMLPGVQBLQDIAVAANPNTVWVUMQGTPPEM-PLDATPAVIQAWYGGN 631
 Db 490 -----GKVKVWLNTGSPLEVASWRDVLQGILLVWQAGO 523

QY 632 ETGNSIAWDVFGDYNPGSKLSSLFPKRLQDNPAFL--NFRTEAEGTLCGEDVYGRY 688
 Db 524 EMGRIVADVLVCKINGSKLPIPTPKDYSWTPGEGKDNPQRVWYEDIVGYRY 583

QY 689 EFADKDVNPFGHGLSYTTFAFNSLVSCHKDGLSVLSVKNTGSGVPGQAQVQLVVKPLQ 748
 ; : | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 584 DTFCVEPAYEFGVGLSYTKEFYDKLTIAIDGETLRVSYTTINHGDRAGKEYSQQVYIK-AP 642
 -TISGFAMATPLSLSELGWWTAPAADIATAKAVESARKATAVFA---YDGTGEGVDRP 1648
 QY 749 AAKTNRPVPELKGSKAFAKE-LQPGFTKAVTIEEQKYVAYFEDERDOWCVEGKDYEVIVS 807
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 643 KGKIDKPKFOELKAFAHKTKLNPOSEEESELETPPLRDLASFDGKE--WVWESGEYEVVRG 699
 QY 808 DSAAKDGVALRGKFTV-GE 826
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 700 ASR---DIRLDIFLVEGE 716
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 RESULT 3 US-09-105-537-4
 ; Sequence 4, Application US/09105537A
 ; Patent No. 6265202
 ; GENERAL INFORMATION:
 ; APPLICANT: Sherman, D.H.
 ; APPLICANT: Liu, H.
 ; APPLICANT: Xue, Y.
 ; APPLICANT: Zhao, L.
 ; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
 ; FILE REFERENCE: 600.438US1
 ; CURRENT APPLICATION NUMBER: US/09/105,537A
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 3782
 ; TYPE: PRT
 ; ORGANISM: Streptomyces venezuelae
 US-09-105-537-4
 Query Match 21.7%; Score 951.5; DB 4; Length 3782;
 Best Local Similarity 31.4%; Pred. No. 1.3e-83; Mismatches 340; Indels 137; Gaps 25;
 Matches 275; Conservative 123; Mismatches 340;
 QY 9 ILLKKTLAEKVDDLAGDFW-----HTKALPKHKGVPSSLRTDGPNGVRGKTFENG 58
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 1121 IVAQMTDEKISFV---HWALDPDRONVGYLPGVPRLGIPELRAADGPNGR---LWG 1172
 QY 59 VPACCPGTSI-GSTFWOTLLEAGKMGKELAIKSAHVIIGPTINMQSPGGFESI 118
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 1173 QTATALPAPVALA-ASTEDTDMAIDSYGKVMGRDGRALNQDMVLPGMNMRVPHGRNYES 1232
 QY 119 GEDPFLAGGAALIRGQISTGVQATTHFLCNDODRRMAMQSVITERAIREYIALPQ 178
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 1233 SEDPLVSSRTAVAQIKGQAGLMTTAKHFAANNQENRNSVANDEQTLREIEPPAF 1292
 QY 179 IAVRDSOPGA- FMTAYNGINGVSCSENPKYLDGMURKEWGDGLMSDWNGYGTSTEAV 236
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 1349 TKGLDQEMGVELPGDVPKGEPSSPAKFGEALKTAVLNGTVEAAVRSARIVGOMEKF 1408
 1293 AS---SKAGAASFMCAYNGLNGKPCSGNDELLNNVRLTQWFGQWMSDWLAT-PGTD 1348
 QY 237 VAGIDLEM-----POPP-RFGETKFNYSNGK-PIHVIDORAREVLOFK 282
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 108 QTATALPAPVALA-ASTEDTDMAIDSYGKVMGRDGRALNQDMVLPGMNMRVPHGRNYES 1408
 QY 283 CAASGVTENGPEVVNTPETAAALLRKVGNEGCVLKNENNVLPLS--KKKTLWGPNA 340
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 1409 GLLIATPAPRPE---RDRGAAVSRKVAENGAVLRLNEGOAALPLAGDAGSKIASIVGPTA 1465
 QY 341 KQATYHGGSAALRAYAYTTPFDGLSKOLETPPSYTGYATTVPPLGECOCTPDGAGM 400
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 1466 WDPKVTLGLGSAAHVVPDSAAPLDTIKAR-----AGAGATVYERGEETGTO 1517 PAGN
 QY 401 RWRYTENEPGPGTPNROHIDELEFLFTKTDMLVYDHHYHPKAADTWADMEGYTADBDCTELG 460
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 1518 ISPAFNG-----HOLE---PGKAGALY--DGILTVWADGERIA 1552
 QY 461 LWVCGTAKAYVDDQLWVNDATKQVPGDAFGSATREERGRINLYVKGNYKIEFEGSAPT 520
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 1553 WRATG---GYATVOL---GSHTIEAGOYVGKVS--SPPLKLJTKG-THKL----- 1592

RESULT 4 US-09-105-537-24
 ; Sequence 24, Application US/09105537A
 ; Patent No. 6265202
 ; GENERAL INFORMATION:
 ; APPLICANT: Sherman, D.H.
 ; APPLICANT: Liu, H.
 ; APPLICANT: Xue, Y.
 ; APPLICANT: Zhao, L.
 ; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
 ; FILE REFERENCE: 600.438US1
 ; CURRENT APPLICATION NUMBER: US/09/105,537A
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 809
 ; TYPE: PRT
 ; ORGANISM: Streptomyces venezuelae
 US-09-105-537-24
 Query Match 21.5%; Score 944.5; DB 4; Length 809;
 Best Local Similarity 32.2%; Pred. No. 4e-84; Mismatches 325; Indels 143; Gaps 26;
 Matches 275; Conservative 112; Mismatches 325;
 QY 9 ILLKKTLAEKVDDLAGDFW-----HTKALPKHKGVPSSLRTDGPNGVRGKTFENG 58
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 56 IVAQMTDEKISFV---HWALDPDRONVGYLPGVPRLGIPELRAADGPNGR---LWG 107
 QY 59 VPACCPGTSI-GSTFWOTLLEAGKMGKELAIKSAHVIIGPTINMQSPGGFESI 118
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 108 QTATALPAPVALA-ASTEDTDMAIDSYGKVMGRDGRALNQDMVLPGMNMRVPHGRNYES 107
 QY 119 GEDPFLAGGAALIRGQISTGVQATTHFLCNDODRRMAMQSVITERAIREYIALPQ 178
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 168 SEDPLVSSRTAVAQIKGQAGLMTTAKHFAANNQENRNSVANDEQTLREIEPPAF 227
 QY 179 IAVRDSOPGA- FMTAYNGINGVSCSENPKYLDGMURKEWGDGLMSDWNGYGTSTEAV 236
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 284 TKGLDQEMGVELPGDVPKGEPSSPAKFGEALKTAVLNGTVEAAVRSARIVGOMEKF 343
 QY 228 AS---SKAGAASFMCAYNGLNGKPCSGNDELLNNVRLTQWFGQWMSDWLAT-PGTD 283
 QY 237 VAGIDLEM-----POPP-RFGETKFNYSNGK-PIHVIDORAREVLOFK 282
 ; : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 284 TKGLDQEMGVELPGDVPKGEPSSPAKFGEALKTAVLNGTVEAAVRSARIVGOMEKF 343
 QY 283 CAASGVTENGPEVVNTPETAAALLRKVGNEGCVLKNENNVLPLS--KKKTLWGPNA 340

Db 344 GLIATPATPAPRE--RDKAGAQAVSRKVAENCAVLLRNNEGAOLPLAGDASKIAVIGPTA 400
 Qy 341 KOAHYHGGSAIRAYVVTPEGLSKOLETPPSYIVGATTVPPLIGEOCLTPDGAPM 400
 Db 401 VDPKVTLGLGSAHVWVPSDSAAPLDTIKAR-----AGAGATVYETGEETFGTQIPAGN 452
 Qy 401 RWRVFNEPGTPNRQHIDELFFTKTDMLHVDYHPKAADTYWADMEGTYTADEDCTYELG 460
 Db 453 LSPAFNQG-----HOLE---PCGAGALY--DGTEVTPAGEYRIA 487
 Qy 461 LWVGCTAKAVYDQLVVDNATKQVPGDAFFGSASTREETGRINLVGNTRYKFKIERSAPT 520
 Db : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 488 VRATG--GYATVQL---GSHTIEAQVQIKVS--SPULKLTGK-TKRL----- 527
 Qy 521 YTAKGDTIVPGHSLRVGGCKVTDQAEETRSVALAKEHQVITCAGLNADWETEGADRA 580
 Db 528 -TISGFAMSATPLSLEGPWVPAADATIAKAVESARKARTAVVFA--YDGTEGVDRP 583
 Qy 581 SMKLPGVGDQLADVAANPNTVWVWVQGPPPEEMWLDATPAVTOAWGGNETONSIADV 640
 Db 584 NLSLPGFDKLISIADANPNTIVWVNGSSVLMFWLSKTRAVLDMWYQPGQAETAA 643
 Qy 641 VPGDYNISGSKLISFVKRLQDNPAFLNFRERAG-----RILYGEDVYVYRIF 690
 Db 644 LRDVNPSPGKLUQSF-----PAEONQHAWAGOPTSPYGVQDNGOTYPREGIVGYRFK 696
 Qy 691 AUKDVWEPFGHLSYTTFASPNLSYH-KDGKLSVSLSYKNTGSVPGQVAOLYVKPLQ 749
 Db 697 ENVKPLPFPGHLSYTFSQTOSAPTVRTSGKGKVTVTRNSKRAGGEVUVQAYLGASP 756
 Qy 750 AKRNDGVALRKFKFTV 824
 Db 757 VTAPOAKKKVGYTRYSLANGEAKTVTVNV-----RRQLOQTS 795
 Qy 810 SAKDGVALRKFKFTV 824
 Db 796 SSAD---LRQSATV 806

RESULT 5

; Sequence 7, Application US/09147236A

; GENERAL INFORMATION:
; ; Patent No. 6316251;
; ; APPLICANT: TONOUCHI, Naoto
; ; APPLICANT: TSUCHIDA, Takayasu
; ; APPLICANT: YOSHINOYA, Fumihiro
; ; APPLICANT: TAHLA, Naoki
; ; APPLICANT: HAYASHI, Takahisa
; ; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
; FILE REFERENCE: 6537-011-OPT
; CURRENT APPLICATION NUMBER: US/09147,236A
; CURRENT FILING DATE: 1999-04-08
; EARLIER APPLICATION NUMBER: PCT/JP97/03363
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 735

; TYPE: PRT
; ORGANISM: Acetobacter xylinum
; FEATURE:
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, or
; ; OTHER INFORMATION: c

Query Match 19.6%; Score 860; DB 4; Length 735;
 Best Local Similarity 28.3%; Pred. No. 7_9e-76; Mismatches 277; Indels 210; Gaps 22; US-09-147-236-7

Db 46 GPNGVRGKFF--NGVACFPCCGHSLSGSTFNQTLLEEGKMMCREATAKSAAHVLGPTI 103
 Qy 46 GPNGVRGKFF--NGVACFPCCGHSLSGSTFNQTLLEEGKMMCREATAKSAAHVLGPTI 103
 Db 97 AGIGVRRPHIRRG-EAVSLPSGOSTASTWDMDMARQAGVMGREAWQSGNFNILLGGAA 155
 Qy 104 NHMRSPGPGGRGPFESTICBDPELAGLGAALTRGIOSTGVOATKIFLCNOEDRMMVOSI 163
 Db 156 DLTRDPKGGRNFPEYAGEDPLOTGRMVGSTAGVOSQHVISTLKHYAMNLDLETSRMTSAD 215
 Qy 164 VTERALAREYALPEFOAVRISQSGAFTMAYINGINGVSCSENPKYLDGMURKENGWDGIM 223
 Db 216 IDPVAMKESDLIGFEIATEGTGHPGAMCSYRNVDLYACENPYLLNKTKIOPWHYPGRM 275
 Qy 224 SWWGYSTSTEAVWAGLDLEMPGP----PRFSETLKENVSNC-KPPIHVIDQAREVL 277
 Db 276 SDWGATHSSARALAAGLDQESAGDHTDARYPR-TLAADAVKAGRVRBARNDAER--- 331
 Qy 278 QFVKKAACSTEN---GETTWNIPSTAAUULKVGENGTULKHNENVNLPSKRT 333
 Db 332 -VVRALFAAGLVDHDPQAGBLDPLWDVYDT---LVAQKDDEEGAVLRLRNQGNIILPSARI 386
 Qy 334 LIVGPWAKQATYHGGGSALRAYYAVTPDGLSKOLETPPSYVPGAYITVPPILGQCLT 393
 Db 387 AVIGSHADAVISGGS-----SQVDPIGGE--- 412
 Qy 394 EDDGAPMWRVNEIPPGTPNRQHIDELFFTKTDMLHVDYHPKAADTYWADMEGTYADE 453
 Db 413 ----- 412
 Qy 454 DCTYELGLVYVCGTAKAVYDQLVVDNATKQVPGDAFFGSASTREETGRINLVGNTRYK 513
 Db 413 -----AVKGPSK-----KEWPGDPV----- 428
 Qy 514 EFGSAPTYVILKGDITVPGHSLRVGGCKVDDORETEKSVALAKEHQVITCAGLNADWE 573
 Db 429 -FPPSPLKQAMOE-APG---ARL---TYDCTSTIASARARAADVVVVA---TQFT 475
 Qy 574 TEGADRASKLPGVLDQLADVAANPNTVWVWVQGPPPEEMWLDATPAVTOAWVGGNET 633
 Db 476 FEGMDAPSMDNNADALTAVAAANPNTVWVWVNETGDPVLMWNSSVAGYLEAWPPGSG 535
 Qy 634 GNSTADWVPGDYNPSGKLSLSEFPLR-----LQDNPALMFTRTGRTYGEW 681
 Db 536 GPATARLLEGKVAPSGHMTMTPQAESQLAHDPIAGWTADANFEMOFHTQ-ELVYDEGS 594
 Qy 682 YVGTRYEEADKVNPFPGHLSYTTFASPNLSYH-KDGKLSVSLSYKNTGSVPGQVAQ 741
 Db 595 DVGRWFDRDHFKPLPFGYGLYTTFSTDGKVTRHGGQVATVNHNTRAGDVQ 654
 Qy 742 LYVKPLQAKKINRPVKEKLGFAKVELQPGTAKVTFEQKVYAYFDERDQNCVEKD 801
 Db 655 VYV-----GLPDGARRLAGWORISLAPGESROSV-OLEPRLLAHFDGHDWRNSVPSGT 708
 Qy 802 YEVIVSDSSAAKD 814
 Db 709 FRVWL-ASCATD 719

RESULT 6

; Sequence 2, Application US/08462080B
; Patient No. 5991913
; GENERAL INFORMATION:
; ; APPLICANT: Fowler, Timothy
; ; APPLICANT: Barnett, Christopher C.
; ; APPLICANT: Shoemaker, Sharon
; ; TITLE OF INVENTION: Saccharification of Cellulose by Cloning and Amplification of the Beta-glucosidase Gene of Trichoderma R NUMBER OF SEQUENCES: 4
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: Genencor International, Inc.
; ; STREET: 925 Page Mill Road
; ; CITY: Palo Alto

STATE: Ca
 COUNTRY: U. S. A.
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/462,080B
 FILING DATE: 05-JUN-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/248,586
 FILING DATE: 24-MAY-1994
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/807,028
 FILING DATE: 10-DEC-1991
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/625,140
 FILING DATE: 10-DEC-1990
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Stone, Christopher L.
 REGISTRATION NUMBER: 35,696
 REFERENCE/DOCKET NUMBER: GCT78D3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-845-6504
 TELEXFAX: 650-846-7555
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 744 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-462-080B-2

Query Match 16.7%; Score 731.5; DB 2; Length 744;
 Best Local Similarity 27.5%; Pred. No. 4.4e-63;
 Matches 234; Conservative 123; Mismatches 282; Indels 211; Gaps 31;

QY 7 EATIUKTLAKVVDLALIGFW-----HTIKALPKHGVISLRFDTGPNGNR---GKTF 55
 Db KAALAKLNQDVKVIGVG---WNGGPVCVGHNSPASKRISYSLCQDGLGVRYSTGCAF 106
 Qy 56 FNGVWACFCFGTSGLSTFPQTLLEAGKAMKEIAKSAAHVLGPTIN-MORSPLGGRS 114
 Db 107 TPGVQAA-----STWVNLRLERGOIGEEVKAASGTHVILGPVAGBLGKTPQGRN 157
 Qy 115 FESI1EDPFPFLAGLAALIRGIQSTQVATKHFCLNDQDERRMMVQSIINTERAIREYA 174
 Db 158 WEGFGDVPLGTYGIANQCTINGIQSYGVQATAKHYTLINEQELRETISNNDDRTLHELYT 217

Qy 175 LPFOJAVRDSOPGAMTAYINGINGYCSCEPKYQKYLQMLRKEWGWGLIMDWYGYSTTE 234
 Db 218 WPFADAVO-KANVASYMCSYNKRNTWACEDQYLTQVLUKQDQLGFFGYVMIDWNAOHTVQ 276

Qy 235 AVWAGDLERPGPP-----RFRGEULKFNV--SNGKPFPIHVIDQARAREVLOFVKKAASGV 288
 Db 277 SANSGLDMSPGTGDFENGNNRLWGPALTNAVNSNOOPTSRVDM---VTRLAANWLTGQ 332

QY 289 TENG-PETVNNTPE-TAALLRKVNEGIVVLLKHNENNVPISKRRKTLTVGPNAQATY 345
 Db 333 DQAGYPSFNISRNVQGNHKITNVRATRDGTIVLKLNDANILPLKKPASIAV----- 383

Qy 346 HGGGSIALRALRAYAVTFPDGLSKOLEMPPEPSYTGAVTIVPPIGLG-CLTDPGAPGRWRV 404
 Db 384 ---GSRAI-----IGNHARNRSPSCNDGCC-DDGALGKGW- 413

405 FNEPCGTPNROHIDELFTKTIDMHLDVYIYKPAADTWAMEGTIVADECTYELGLWV 464

Db 414 ---GSGAVVNYP-----FVAPYDAILNTRASSGQ- 439

Qy 465 GTKAVVDDOLYVTDNATKOVPGDAFFGSAATREBTGIRNLVKGNTYKFIERSAPTYLK 524
 Db 440 -----QVTLNTNDNTSSG---ASAARGKDVAIVFTADS----- 470

Qy 525 GDTIVPHGSLRVGGCKVDDOAETEKSVALAKEHHDQVTCAGINANMWECEADRSMKL 584

Db 471 -----GEGYITVEG--NAGDRNRL----- 495

Qy 585 PGVLQDJIAVVAANPNVVMQNTGTP---EEMPWIDATPAVIOAQWVYGGNETGNSIADV 641

Db 496 -----IYQAVAGANSNVIVVHSVAGILELALQKVAVWAGLPSQESGNALWDVL 549

Qy 642 FGDDYNPSGKLSLSFPKRQLDNPAFLNR-TEAGRTLYGEDVVYGVYRYEFADKDVNFPPG 700

Db 550 WGDVSPSGKLVVTIAK---SPNDYNTRIVSGSDSFSEGFLFDYKHEDCANITPRYEFQ 605

Qy 701 HLSYT"FAFSNLSV- SHKDGS-----USLSLSKNTGVPGQVQAQ 741

Db 606 YGLSYTQRKNYSRSLVUSTAKSGPATGAVVPGGSPDSLFDONVATVTDANSQYTT3AEVAQ 665

Qy 742 LYV-KPIQAKINRPVELKGAKEVQPGETKAVTIEQEKVVAFDEERDQWCEKG 800

Db 666 LYTYPPSAPR-TPPKOLRGPAKLNUTPGOSQTATNMRRLD-SWDTASQKWVPSG 722

Qy 801 DYEVIVSDSS 810

Db 723 SRGISVGASS 732

RESULT 7
 US-08-462-090-2
 Sequence 2, Application US/08462090
 ; Patent No. 6022725
 ; GENERAL INFORMATION:
 ; APPLICANT: Fowler, Timothy
 ; APPLICANT: Barnett, Christopher C.
 ; APPLICANT: Shoemaker, Sharon
 ; TITLE OF INVENTION: Saccharification of cellulose by Cloning
 ; TITLE OF INVENTION: and Amplification of the Beta-D-glucosidase Gene of
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Burns, Doane, Swecker & Mathis
 ; STREET: George Mason Building, 699 Prince St.
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/462,090
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/625,140
 FILING DATE: 10-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Dillahunt, T. Gene
 REGISTRATION NUMBER: 25,423
 REFERENCE/DOCKET NUMBER: 010055-056
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-7400
 TELEFAX: 415-854-8275
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 744 amino acids
 TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-090-2

Query Match 16.7%; Score 731.5; DB 3; Length 744;
Best Local Similarity 27.5%; Pred. No. 4.4e-63; Mismatches 282; Indels 211; Gaps 31;
Matches 234; Conservative 123; MisMatches 282; Indels 211; Gaps 31;

QY 7 EAIKKLTIAEKKVLLAGIDFW-----HTKALPKHGVPSLRFDTGPNGVR---GTFK 55
Db 48 KAALAKLNQDKGVIVSGVG-WNGPCVGNTSPASKISYPSCLQDGPLGVRYSTAF 106

QY 56 FNGVPAACFPCGTSLGSTFNOTLLEAGKMKKEAKSAHVIKGPTIN-MORSPLGG 114
Db 107 TPGVQAA-----SIWDVNLRERGQFIGEVKAQSHIHLGVPLGVKTFQGGRN 157

QY 115 FESIGEDPFLAGLAALIRGIOSTGVQATIKHFLCNDQEDRMMVOSIVTERALREYA 174
Db 158 WPGFGVDPYLITGAMGOTINGIOSVGVQATAKHYILNEOELNRETISNPDDRTHLYT 217

QY 175 LPFOQAVRDSQGFMAYINGVSCSENPKYLDGMRLKREWGDGLIMSDWYGJYSTIE 234
Db 218 WPFADAVQ-ANVASVMSYCYNKVNTWACEDQYLTQVILQDQFGLFGYVMDWNAQHTVQ 276

QY 235 AVVAGLDLEMPPR----REFGETLKENV-SNGKPIHVIDQRAEVQFVKKAASGV 288
Db 277 SANGLDMMSMPGTDNGNNRMLWPALTNVNSQVPTSRVDDM---VTRILAAWLITGQ 332

QY 289 TENG-PETVNNTPPE-TAALLRKVGNEGVILKVENNVLNPUSKKKTLIVGPNAQATY 345
Db 333 DQAGYPSFNISRNVQGNHKTNRVIA RDGTVLKLKDNDLPLKKPASIAV----- 383

QY 346 HGGSAALRAYAVTPFDGLSKOLEPPSFTVPGQ-CLTPDGAPGMRWRV 404
Db 384 --GSAAI-----IGNHARNSPSCNDKGC-DDGALGMW- 413

QY 405 FNEPPGTPNQHDLDELFPTKIDTMHLVDYHKAADTWADMEGTYTADEDCTYELGLVVC 464
Db 414 --GSGAVNYP-----FVAPYDAINTRASSQGT----- 439

QY 465 GRAKAYVDOLVNDNATKQVQGDAFFSATRETRGRINLVKGNTYKFKEFGSAPTYLK 524
Db 440 -----QVLSNNTNTSSG---ASARQKDVAVFTADS----- 470

QY 525 GTDITVPGHGSIVVGGKVKVQDPAETKSVALAKEHQDVTICAGLNAWDWETEGADRASMLK 584
Db 471 -----GEGYITVEG--NAGDRNND-----PWHNGNA----- 495

QY 585 PQLDQLJADVAANNTVUMQTP--BEMPWIDATFQVIAQWGGNETGNSIADV 641
Db 496 -----LVOAVAGANSNVIVVTHSGAILBOQIALPOVKAVVWAGLPLPSQESGNALVDL 549

QY 642 FGDYNNPSGKLSISFPKRQLQDNPAFLNFR-TEAGRITYGEDVYVGYYEFADKDVNFPFG 700
Db 550 WGDVSSESGKLVYTAK---SPNDYNTRVSGPSDFSEGFLDVKHFDDNNTPRYRC 605

QY 701 HGLSYTPEFAENLSV--SHDKG-----LSVLSVSKWNGVGAQVQ 741
Db 606 YGLSYTKFNYRSLSVLSTAKSGPATGAVVPGPSDLPONVATVTDIANNSQVQGAEVQ 665

QY 742 LYVK-PLQAQKINRPKEKFLQPESETKATIEEOKVAYADEFERDORQVKG 800
Db 666 LYVYTPSSAPR--TPPKQQLRGFAKLNLTQPGQSGTATNIRRDL-SYWDTASQKWWPSG 722

QY 801 DVEVIVSDSS 810
Db 723 SFGISVQASS 732

; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; APPLICANT: Barnett, Christopher C.
; APPLICANT: Shoemaker, Sharon
; TITLE OF INVENTION: Saccharification of cellulose by Cloning
; TITLE OF INVENTION: and Amplification of the Beta-glucosidase Gene of
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS: Genencor International, Inc.
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94304-1013

; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 35,696
; REGISTRATION NUMBER: GC7BD4
; REFERENCE/DOCKET NUMBER: GC7BD4
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Christopher L. Stone
; REGISTRATION NUMBER: 35,696
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-6504
; TELEFAX: 415-845-6504

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; US-08-462-461-2

Query Match 16.7%; Score 731.5; DB 3; Length 744;
Best Local Similarity 27.5%; Pred. No. 4.4e-63; Mismatches 282; Indels 211; Gaps 31;
Matches 234; Conservative 123; MisMatches 282; Indels 211; Gaps 31;

QY 7 EAIKKLTIAEKKVLLAGIDFW-----HTKALPKHGVPSLRFDTGPNGVR---GTFK 55
Db 48 KAALAKLNQDKGVIVSGVG-WNGPCVGNTSPASKISYPSCLQDGPLGVRYSTAF 106

QY 55 FNGVPAACFPCGTSLGSTFNOTLLEAGKMKKEAKSAHVIKGPTIN-MORSPLGG 114
Db 107 TPGVQAA-----SIWDVNLRERGQFIGEVKAQSHIHLGVPLGVKTFQGGRN 157

QY 115 FESIGEDPFLAGLAALIRGIOSTGVQATIKHFLCNDQEDRMMVOSIVTERALREYA 174
Db 218 WPFADAVQ-ANVASVMSYCYNKVNTWACEDQYLTQVILQDQFGLFGYVMDWNAQHTVQ 276

QY 235 AVVAGLDLEMPPR----REFGETLKENV-SNGKPIHVIDQRAEVQFVKKAASGV 288
Db 277 SANGLDMMSMPGTDNGNNRMLWPALTNVNSQVPTSRVDDM---VTRILAAWLITGQ 332

QY 289 TENG-PETVNNTPPE-TAALLRKVGNEGVILKVENNVLNPUSKKKTLIVGPNAQATY 345
Db 333 DQAGYPSFNISRNVQGNHKTNRVIA RDGTVLKLKDNDLPLKKPASIAV----- 383

QY 346 HGGSAALRAYAVTPFDGLSKOLEPPSFTVPGQ-CLTPDGAPGMRWRV 404
Db 384 --GSAAI-----IGNHARNSPSCNDKGC-DDGALGMW- 413

QY 405 FNEPPGTPNQHDLDELFPTKIDTMHLVDYHKAADTWADMEGTYTADEDCTYELGLVVC 464

RESULT 8
; Sequence 2, Application US/08463461
; Patent No. 6103464

Db 414 --GSGAVNVPY-----FVAPYDAINTRASSQGT----- 439
 QY 465 GTAKAYVDQQLVNDATKQVPGDCAFFGSAATREETSGRINLYKGNYKFKEFGSAPTYLK 524
 Db 440 -----QVLSINTNTSSG----ASAARGKDVIAVFTADAS----- 470
 QY 525 GDTIVPGHSLRVGGCKVIDDQAIEKSVALAKEHDHQVILCAGLNADWETEGADRASML 584
 Db 471 -----GCGYITVEG--NAGDRNLD----- 495
 QY 585 PGVLQDILADVAANPNTVWVWMTGTP--BEMPDATPAVIAQAWYGGNETGNSIADV 641
 Db 496 -----LVOAVAGANSNVIVVVHSVGAILEQILALPOVKAWVAGLPSQESGNALVVL 549
 QY 642 FGDDNPGSKLUSLSPKRLODNEAFLNR-TEAGRPLYGEDYVGTRYEPADKVNFPG 700
 Db 606 YGLSYTKFVNSRLSVLSTAKSGPATGVWPGGBSDLFQNVAWTVDIANSQVTGAEAQ 665
 QY 742 LYVK-PLOAKTINREPKELKGFKVELQPGEKAVTIEQEKKVVAAYDEERDQMCVEKG 800
 Db 666 LYIYIPSSAPR-TPPKQLRGFAKLNLTPGQSTATINRRLD-SWDTASQWVTPSG 722
 QY 801 DYEVTVSDD 810
 Db 723 SFGISVGASS 732

RESULT 9
 US-08-981-446B-3
 ; Sequence 3: Application US/08981446B
 ; Patent No.: 6300112
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: No. 6300112el beta-xylosidase, nucleotide sequence
 NUMBER OF SEQUENCES: 3
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/981,446B
 FILING DATE:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 804 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Aspergillus niger (CBS 120.49)
 STRAIN: NW147
 FEATURE:
 NAME/KEY: sig-peptide
 LOCATION: 1..26
 ; US-08-981-446B-3

Query Match 9.9% Score 433.5; DB 4; Length 804;
 Best Local Similarity 22.2%; Pred. No. 1.7e-33;
 Matches 200; Conservative 131; Mismatches 276; Indels 293; Gaps 36;

Db 155 TASTISTOGRAFNACRGYLDWYADNINTFRHPWGRCGETPGEDVSLAAVAYEYTGI 214
 QY 137 Q-----STGQATIKHFLNDQED---RRMMYOSIVTERALEREIYALPFQAVRSQP 186
 Db 215 QCPDPESNLKIAATAKHYAGYDIENWHNSRLGNDMNTQODSEYYIPOFHARDKV 274
 QY 187 GAFMAYVINGVSCSENPKYLDGMIRKEWK--DGLIMSDWGYT----- 230
 Db 275 QSMCAVNANGVPCADSYFLOTLRLDTFGFVHDYVSSDCDAAYNINPHGASSQA 334
 QY 231 STTEAVWAGLDLEMPGPFRFGETLKFENSNKGPKIHVIDOREVLQVKCAGTC 290
 Db 335 AAEEAIILAGTDIC-----GTTOWHLNESS--IAQDLSDRDIQEVIRLTTVQA 384
 QY 291 N--GPETVNIP-----ETA--LIRKGNEGIVLKNENNVIPLSKKKTLV 336
 Db 385 GYFDNSNTKANNPYRDLWSVDLETDAWNNSYOAATQGINVLKNSNNVPLTE----- 438
 QY 337 GPNKAQATYHGGSAALRAYVAVTPFDGLSKOLETPSYTGAUTVPPPLGEOCLTPOG 396
 Db 439 -----AY----- 452
 QY 457 YELGLWVCGTAKAYVDDQLVNDATKQVPGDAFFS-----ATREETG-RINLVGN 507
 Db 455 -----NATQOLGN-YYGNAPYMSIPRAAFEACYKVNAEQT 491
 QY 508 TYKFKIEFSSAPTYLKGDTIVPGHSLRVGGCKVIDDQAIEKSVALKHQVITAC 567
 Db 492 -----GISSTST----- 519
 QY 568 LNADMETEGADRASKLPGVLDQTLADYA-AAPNPNTVVMQGTPPEEMPWDAT-----
 Db 520 IDNTTAAEALDRESTAWPGNQDILQIKLASAKKPLIVLQMGQ-----DSSSLKNT 575
 QY 621 --PAVQAWGGNETGNSIADFVWPGMSPKL-SLSPR-KRLQDNPAF-LNFRTEART 675
 Db 576 NVSALLWGGYGPQSGGFALKDITGKKNPAGRVTQVPSAEEFPATDMNLRE----- 631
 QY 676 LYGEDYVGCYRYERADKUNFPCHGSLYSTTAFNSNLSVSHKDGSV----- 724
 Db 632 --GDNPGOTYKWW--TGEAVYEEGHGLFTTFEAESSNTTKEVKLNIDQILSQTHDL 686
 QY 725 -----SLSVKNTGVSVPQGAQVQLYVKPQAAKRNPRYKELKFKA KV-ELQGET 772
 Db 687 ASITQLPVLNTIANTRNGKLESYDTPAMPFANTSDAGPAPYPPKWLGVMDRIGEVKGET 746
 QY 773 KAVTIEQEKKVVAAYDEERDQMCVEKGDYEVIVSDSSAKDGVALRGKFVGETYMSG 832
 Db 747 RELRVPVEGSPARV-NEGDWVWVPGTEBLANLNRKVVKVLEGEEV- VLKWPG 802

RESULT 10
 US-08-386-727-6
 ; Sequence 6: Application US/08386727
 ; Patent No.: 5795647
 GENERAL INFORMATION:
 APPLICANT: ROSEMAN, SAUL
 APPLICANT: BASSLER, BONNIE
 APPLICANT: KEYHANI, NEMAT O.
 APPLICANT: CHITALRU, EDITH
 APPLICANT: ROWE, CHRIS
 APPLICANT: YU, CHARLES
 TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 STREET: 1100 NEW YORK AVENUE, N.W.
 STATE: D.C.

COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,727
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hobbs, Ann S.
REGISTRATION NUMBER: 36,830
REFERENCE/DOCKET NUMBER: 4130/206916
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-386-727-6

Query Match 3.0%; Score 132.5; DB 1; Length 328;
Best Local Similarity 23.4%; Pred. No. 0.00022;
Matches 62; Conservative 37; Mismatches 103; Indels 63; Gaps 9;
Matches 62; Conservative 37; Mismatches 103; Indels 63; Gaps 9;

QY 65 PCCTSLGGTFFNOT-LIFEAGKMGKEIAKSAHVLGPTIN-MORSPLGGRGREGGED 121
Db 78 PCAQLYRSIDNGTQLAEDGGWLMMAELIADIDLSFAPVLDKGFDCAIGNRAF--GDD 134
QY 122 PELAGLGAALTRGISTGVQATIKIF-----LQNQDQDRRMVQSVITERALR 170
Db 135 VQVLTLYSSATVRGMGSVGMATGKHFPGHGAVIDASHLIEPTPYERDSIADDMTFRAOI 194
QY 171 EYALPPOIAVR-----DSQGAMTYAYINGVSCSENPKYLDGMKREKGWDGLMS 224
Db 195 EGILDAMMPARHVTPHYDQ-----ASGSPYWKQVLRQELQFGIVFS 240
QY 225 DWYGTSTTEAVVAGLDLEMFGPPRFERGETLKFNNSNKPFIHVIDQARREVQFVKCA 284
Db 241 D-----DLSEGAATIMGGPAAQOS-----LDAGCDMVLMCNKRES 277
QY 285 ASGVITENGPEPTVNVPETALLRK 309
Db 278 AVAVIDQQLPISVW--PQAOSLLQ 299

RESULT 11
US-08-600-452A-6

Sequence 6, Application US/08600452A
Patent No. 598564
GENERAL INFORMATION:
APPLICANT: ROSEMAN, SAUL
APPLICANT: BASLER, BONNIE
APPLICANT: KEYHANI, NEMAT O.
APPLICANT: CHITLARI, EDITH
APPLICANT: ROWE, CHRIS
APPLICANT: YU, CHARLES
TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTY: USA
ZIP: 92037

RESULT 12
US-09-071-035-458

; Sequence 458, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9110 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
SEQUENCE CHARACTERISTICS:
LENGTH: 2032 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-458

Query Match 2.9%; Score 128.5; DB 4; Length 2032;

Best Local Similarity 20.0%; Pred. No. 0.015; Mismatches 126; Conservative 81; Indels 197; Gaps 31; Matches 227

QY 227 YGTYSGT-----TPEAVVAG--LDLEMGPGRPRGETLKFVNSNGK-PFIH 267
Db 295 YGYTYSIEDGTWVFTFNERITSESDIHGDFSLDTHL-----NDSDGRGPDW 341

QY 268 VTDORAREVLOFVKCASAASGVYENGPEPTVNTPETALLRKVG-----EGIVLKN 320
Db 342 VIDIPTQEDL-----PPVVIPIVDPDEQOIDKGHDRTPNPSAITWVD 386

QY 321 ENNVPLPLSKKKTLIVGPNAKOATYHGGSAALRAYAATVFDGLSKOLE--TPSYTV 377
Db 387 INQAM---KDQT--NPVUTEWPTGVFKPSKVYKVLVNLIDGTKEVRELLSPDYTV 439

QY 378 G-----AY----TIVVPLIGEQTIPDGAPGMWRVF-----NEPPGTPN 413
Db 440 DKGNVNTIKGDTNKAYLEYQFTI-----DEAVIPDGDDGVFPKHNATLTSDDNNPGLDA 494

QY 414 ROHIDELFFKTDMHLVYHPKAADTWADMGTYTADEDCTYELGLVWCGTAKAYVDD 473
Db 495 EATVTATGKMLDRNIDYDEANQETW-----EINNYGEQTIPDKQAVITD 542

QY 474 QLVVDNATKQPGKAFFSATRBTGR---INLVKGNTYKFKIEFGSAPTYTLKGDTIV 529
Db 543 TM-GNLITE-PSDLHLVSFTEDKGNGNEVGABLVEGDKY-----VII 584

QY 530 PGHGSLR----VGGCKVIDDAE---IEKVALAKEHDOVIVICAGLNADMETEGADR 579
Db 585 NGDSFAIDFLHDYTGAVKIDYKTKVGDVAV--NNRVDVGTQHOSEDDGTASQO 641

QY 580 ASMLKLPVIDD---QLIADVAANPNTVV--MOTGTEPEMWLDATPAVQAWGGNET 633
Db 642 NIKMGAVDQYONSP-----IGWTIAVQNLYNLENAVAATDTPVPGCLTMVP----- 689

QY 634 GNSIAUWFGDYPNPSGKLSTSFKRLQDNPAFLNFRTEAERTGKLGEDVYGYR---Y 687
Db 690 -NSL--VVKDTTGAQLTG-----KOFWEITRNADGE--TGFKVSEFQAY 731

QY 688 YEFADKDVNPFPGHGLSYYTFASFLNSLVSVKHDKGLSVLSVKVINGSVPGQAQVQLYVPL 747
Db 732 ARTSD-----AFHITYTF---FDVFIELDANNPDLHYRNTAAIDWDEA---GNN 776

QY 748 QAKAKINRPVKELKGAKEVLOPGETKAVTE 778
Db 777 HHSEDSKPKPLPAFDLNAOKSGVYNAVTKE 807

RESULT 13
US-09-071-035-452
; Sequence 462, Application US/09071035

Patent No. 6448043

GENERAL INFORMATION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MS DOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
SEQUENCE CHARACTERISTICS:
LENGTH: 2032 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-462

Query Match 2.9%; Score 128.5; DB 4; Length 2032;

Best Local Similarity 20.0%; Pred. No. 0.015; Mismatches 126; Conservative 81; Indels 197; Gaps 31; Matches 227

QY 227 YGTYSGT-----TPEAVVAG--LDLEMGPGRPRGETLKFVNSNGK-PFIH 267
Db 295 YGYTYSIEDGTWVFTFNERITSESDIHGDFSLDTHL-----NDSDGRGPDW 341

QY 268 VTDORAREVLOFVKCASAASGVYENGPEPTVNTPETALLRKVG-----EGIVLKN 320
Db 342 VIDIPTQEDL-----PPVVIPIVDPDEQOIDKGHDRTPNPSAITWVD 386

QY 321 ENNVPLPLSKKKTLIVGPNAKOATYHGGSAALRAYAATVFDGLSKOLE--TPSYTV 377
Db 387 INQAM---KDQT--NPVUTEWPTGVFKPSKVYKVLVNLIDGTKEVRELLSPDYTV 439

QY 378 G-----AY----TIVVPLIGEQTIPDGAPGMWRVF-----NEPPGTPN 413
Db 440 DKGNVNTIKGDTNKAYLEYQFTI-----DEAVIPDGDDGVFPKHNATLTSDDNNPGLDA 494

QY 414 ROHIDELFFKTDMHLVYHPKAADTWADMGTYTADEDCTYELGLVWCGTAKAYVDD 473
Db 495 EATVTATGKMLDRNIDYDEANQETW-----EINNYGEQTIPDKQAVITD 542

QY 474 QLVVDNATKQPGKAFFSATRBTGR---INLVKGNTYKFKIEFGSAPTYTLKGDTIV 529
Db 543 TM-GNLITE-PSDLHLVSFTEDKGNGNEVGABLVEGDKY-----VII 584

QY 530 PGHGSLR----VGGCKVIDDAE---IEKVALAKEHDOVIVICAGLNADMETEGADR 579
Db 585 NGDSFAIDFLHDYTGAVKIDYKTKVGDVAV--NNRVDVGTQHOSEDDGTASQO 641

QY 580 ASMLKLPVIDD---QLIADVAANPNTVV--MOTGTEPEMWLDATPAVQAWGGNET 633
Db 642 NIKMGAVDQYONSP-----IGWTIAVQNLYNLENAVAATDTPVPGCLTMVP----- 689

QY 634 GNSIAUWFGDYPNPSGKLSTSFKRLQDNPAFLNFRTEAERTGKLGEDVYGYR---Y 687
Db 690 -NSL--VVKDTTGAQLTG-----KOFWEITRNADGE--TGFKVSEFQAY 731

QY 688 YEFADKDVNPFPGHGLSYYTFASFLNSLVSVKHDKGLSVLSVKVINGSVPGQAQVQLYVPL 747
Db 732 ARTSD-----AFHITYTF---FDVFIELDANNPDLHYRNTAAIDWDEA---GNN 776

QY 748 QAKAKINRPVKELKGAKEVLOPGETKAVTE 778
Db 777 HHSEDSKPKPLPAFDLNAOKSGVYNAVTKE 807

RESULT 13
US-09-071-035-452
; Sequence 462, Application US/09071035

RESULT 14
 Db 642 NIKNTGAVDQNSITGWTLAVNQNYLMENAVITDYEVPGLETWV-::: 689
 Qy 634 GNSIADVFVGDNPSGKLSLSPKRQLDNPAFLNRFTEAGRFLAGEDVVYGR---Y 687
 Db 690 -NSL--WKDITTGQTLIG-----KDFWEITRNADGE--TGFKSFIGAY 731
 Qy 688 YEFADKVNFPGHGLSYTTFAFSNLVSVKHDGKLSVLSVKNQGSGVPGQAQVOLYVPL 747
 Db 732 AKTSD----AFHITYTF---FDVTELDANNPALDHYNRAIDWDEA----GNN 776
 Qy 748 QAKINRPVKEKGAKVELQGETKAVIE 778
 Db 777 HHSEDSKPFPKPLPAFDLNQSKGVYNATKE 807

RESULT 14
 Sequence 466, Application US/09071035
 Patent No. 6448043

GENERAL INFORMATION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071, 035

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: A. Anders Brookes

REGISTRATION NUMBER: 36, 373

REFERENCE/DOCKET NUMBER: PB369P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 466:

SEQUENCE CHARACTERISTICS:

LENGTH: 2032 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-071-035-466

RESULT 15
 Sequence 460, Application US/09071035
 Patent No. 6448043

GENERAL INFORMATION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071, 035

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: A. Anders Brookes

REGISTRATION NUMBER: 36, 373

REFERENCE/DOCKET NUMBER: PB369P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 460:

SEQUENCE CHARACTERISTICS:

LENGTH: 737 amino acids

TYPE: amino acid

US-09-071-035-466

Query Match 2.9%; Score 128.5; DB 4; Length 2032;
 Best Local Similarity 20.0%; Pred. No. 0.015; DB 4;
 Matches 126; Conservative 81; Mismatches 227; Indels 197; Gaps 31;

Qy 227 YGTY-----"TPEAVWAG--LDLEMGPGRPRFRGETLKFNWSNGK-PFH 267
 Db 295 YGYTISEDGTVFTFNERITSESDIHDFSLDTHL-----NDSDGRGPDW 341
 Qy 268 VTDORAREBVLOVKKCASGVTENGTEITVNTPEFAALLRKGN-----EGIVLKN 320
 Db 342 VIDPIOTBDL-----PPVPIPVDPEQIDKQGHFRDTPNPSALTWTWD 386
 Qy 321 ENNVLPLSKKKTLIVPNAKQATYHGGSAALLRAYAVTFDGLSKQE---TIPSYTV 377

STRANDDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-071-035-460

Query Match 2.8%; Score 122.5; DB 4; length 737;
 Best Local Similarity 19.8%; Pred No. 0.0095; Indels 193; Gaps 30;
 Matches 116; Conservative 76; Mismatches 202;

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QY 227 YGTVS-----TTRAWAG--IDLEMPGPPRPRGETLKFNFNSNK-PFIH 267
Db 263 YGTVTISEDGTVRTFNERITSDIHDPSLTHL-----NPSDGRGIGDW 309
QY 268 VIDORAREVLQFWKKCAASGVTEENGPEVTNNTPETAAALLRKGN-----EGIVILK 320
Db 310 VIDIPTQEDL-----PVPVPIPTPDTEQDQGHEDRTPNPSAITWVD 354
QY 321 ENNVLPPLSKKKKLIJVGENAQATYHGGSAALRAYAATPFDLSKOLE--TPPEYT 377
Db 355 INQAM---KDQT--NPVTVETWPTGTNSPKSVKVYELVMNLDTIKEVGRBLSPEITV 407
QY 378 G-----AY-----TVPVPLIGEOCLTPDAPGMWRVF-----NEPPCTPN 413
Db 408 DKNQNVTRKGDTINKAYRLEYQTTI-----DEAVIPDAGGDVPRKHATLTSDNPNGLDA 462
QY 414 RQHIDELFFTKTDMHLVDYUHPKAADTWADMEGYTADECCTYELGLNVCGCTAKAYDD 473
Db 463 EATVTTATYGKMLDRNNTIDEANQEFW-----ELVNNGEOTIPKDKQAVITD 510
QY 474 QLVWIDNATKQVPGDAFFGSATRETRGK----INLVKGNTYKIEGSAAPTWTLKGDTV 529
Db 511 TM-GDNLTPE-PLSHLYSVTFDKGNEWVGAELVEKDY-----WVI 552
QY 530 PGHQSLR-----VGGCKVDDAE---TEKSVALKEREHDVITCAGLNADWETEGADR 579
Db 553 NGDGSFAIDFLHIDWTGAVKIDYTKVKGIVEGDDAV--NNRDVGHQHBRDDGASQQ 609
QY 580 ASMKLPGVLD---QLIADVAANPNTVVW--MQTGTPPEMPWILDATPAVQAWGGNET 633
Db 610 NIKNTGAVDQYQNSTGWTALVQNNYLMENAVITYDTEPVPGLTWVP----- 657
QY 634 GNSTADVVFGDYPSGKUSLSFSKRLQDNPAHNFREBAGRLLIGEDVYVGYR-----Y 687
Db 658 -NSLU---VVKDITPTGAQITLG-----KDFMVEITRNADGE--TGFKVSTGAY 699
QY 688 YEFADKDVNPFEGHGLSLYTFAFSNLVSVKDQKLSVLSVKNTGSV 734
Db 700 AKTSDF-----AFHITYTF---FDVTELDANNPALDHFRNTAAJ 735

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Search completed: April 26, 2003, 13:02:52
 Job time : 27 secs

